

FIGURE 1

MOUSE B7x PROTEIN SEQUENCE

MASLGQIIFWSIINIILLAGAIALIIGFGISGKHFITVTTFTSAGNIGEDGTLSCTFEPDIKLNQIVIQWL
KEGIKGLVHEFKEGKDDLSQQHEMFRGRTAVFADQVVVGNA^{SL}RRLKNVQLTDAGTYTCYIRTS
KGKGNANLEYKTGAFSMPEINVDYNASSE^{SL}RCEAPRWFPQPTVAWASQVDQGANFSEVSNT
SFELNSENVTMKVVS^{VL}LYNVTINNTYSCMIENDIAKATGDIKVTDS^{EV}KRRSQLQLLN^{SG}PSPCV
FSSAFAAGWALLSLSCCLMLR

HUMAN B7x PROTEIN SEQUENCE

MASLGQILFWSIISIIILLAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNAS^{SL}RRLKNVQLTDAGTYKCYIITSKGKGNANL
EYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTV^WWASQVDQGANFSEVSNTSFELNSENVTM
KVVSVLYNVTINNTYSCMIENDIAKATGDIKVTES^{EIK}R^{RR}SHLQLLN^{SK}ASLCVSSFFAISWALLPLSPYL
MLK

FIGURE 2

MOUSE B7x NUCLEIC ACID SEQUENCE

ATGGCTTCCTTGGGGCAGATCATCTTTTGGAGTATTATTAACATCATCATCATCCTGGCTGGGGC
CATCGCACTCATCATTGGCTTTGGCATTTCAGGCAAGCACTTCATCACGGTCACGACCTTCACCT
CAGCTGGAAACATTGGAGAGGACGGGACCCTGAGCTGCACTTTTGAACCTGACATCAAACCTCAA
CGGCATCGTCATCCAGTGGCTGAAAGAAGGCATCAAAGGTTTGGTCCACGAGTTCAAAGAAGGC
AAAGACGACCTCTCACAGCAGCATGAGATGTTGAGAGGCCGCACAGCAGTGTTTGCTGATCAGG
TGGTAGTTGGCAATGCTTCCCTGAGACTGAAAAACGTGCAGCTCACGGATGCTGGCACCTACAC
ATGTTACATCCGCACCTCAAAGGGCAAAGGGAATGCAAACCTAGAGTATAAGACCGGAGCCTTC
AGTATGCCAGAGATAAATGTGGACTATAATGCCAGTTCAGAGAGTTTACGCTGCGAGGCTCCTC
GGTGGTTCCCCCAGCCCACAGTGGCCTGGGCATCTCAAGTCGACCAAGGAGCCAACTTCTCAG
AAGTCTCGAACACCAGCTTTGAGTTGAACTCTGAGAATGTGACCATGAAGGTCGTATCTGTGCTC
TACAATGTCACAATCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCCACTGG
GGACATCAAAGTGACAGATTCAGAGGTCAAAGGCGGAGTCAGCTGCAGCTGCTCAACTCCGG
GCCTTCCCCGTGTGTTTTTCTTCTGCCTTTGCGGCTGGCTGGGCGCTCCTATCTCTCTCCTGTT
GCCTGATGCTAAGATGA

FIGURE 3

HUMAN B7x NUCLEIC ACID SEQUENCE

ATGGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGC
AATTGCACTCATCATTGGCTTTGGTATTTAGGGAGACACTCCATCACAGTCACTACTGTGCGCT
CAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTCT
GATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAA
AGATGAGCTGTCGGAGCAGGATGAAATGTTGAGAGCCGGACAGCAGTGTTTGCTGATCAAGTG
ATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATG
TTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCA
TGCGGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATG
GTTCCCCCAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTTCTCGGAAGTC
TCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAA
TGTTACGATCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATA
TCAAAGTGACAGAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTC
TCTGTGTGTCTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATGCT
AAAATAA

FIGURE 4

[illegible]

B7x	65	N	G	I	V	L	O	V	L	K	E	G	-	-	-	I	K	C	L	V	H	E	F	K	E	G	K	D	I	S	Q	Q	H	E	M	F	R	G	R	T	A	V	F	A	D	Q	V	V	V	G	N	A	S	U	R	I	K	N	V	Q	L	T	D	A	G	T	Y	T	C	J	I	R	T	134	
B7.1	64	S	E	D	R	I	Y	W	O	K	H	D	-	-	-	-	-	K	V	L	S	V	I	A	G	K	L	V	W	P	E	Y	K	N	-	-	R	T	L	Y	D	N	T	T	-	-	-	S	L	I	I	L	G	L	V	L	S	D	R	G	T	S	V	W	Q	K	123								
B7.2	51	S	E	I	V	V	F	W	Q	D	Q	-	-	-	-	-	-	K	L	V	L	Y	E	H	Y	L	G	-	-	T	E	K	L	D	S	V	N	-	-	A	K	Y	T	G	R	T	S	F	D	R	N	W	T	H	R	I	K	D	M	G	S	I	D	G	F	J	I	Q	K	114					
B7h	73	S	G	L	Y	V	Y	W	Q	I	E	N	P	E	V	S	V	T	Y	L	P	Y	K	S	P	G	-	-	I	N	V	D	S	S	Y	K	N	-	-	R	G	H	I	S	L	D	S	M	K	Q	G	N	F	S	L	Y	L	K	N	V	T	P	Q	D	T	O	E	F	T	G	R	V	F	M	142
PD-L1	51	L	A	L	V	Y	W	E	K	E	D	-	-	-	-	-	-	E	Q	V	I	Q	F	V	A	C	B	-	-	D	L	K	P	Q	H	S	N	F	R	G	R	A	S	L	P	K	D	Q	I	L	K	G	N	A	L	Q	I	T	D	Y	K	L	Q	D	A	G	V	Y	C	G	I	I	S	Y	118
PD-L2	53	E	G	I	R	A	S	L	O	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	E	N	-	-	D	T	S	L	Q	-	S	E	-	-	R	A	T	L	E	E	Q	L	P	L	G	A	L	F	H	I	P	S	V	Q	V	R	D	S	Q	O	X	R	G	L	V	I	C	106		
B7-H3	61	A	Q	I	N	L	I	W	O	L	T	D	-	-	-	-	-	T	K	Q	L	V	H	S	F	T	E	G	R	-	D	Q	G	S	A	Y	S	N	-	-	R	T	A	L	F	P	D	L	V	Q	G	N	A	S	U	R	I	K	N	V	Q	L	T	D	E	G	S	Y	T	C	F	V	S	I	126

B7x	135	S	K	G	K	-	-	-	-	-	-	-	-	E	I	N	-	V	D	N	A	S	-	-	E	L	R	C	E	P	R	W	F	I	P	T	M	A	V	A	S	Q	V	D	Q	G	A	N	F	S	E	193																													
B7.1	124	K	E	R	G	T	Y	E	V	K	H	L	A	L	V	K	I	S	I	K	A	I	R	A	D	F	F	S	T	-	-	-	-	-	-	P	N	I	T	E	S	G	N	S	A	D	T	K	R	I	T	C	F	A	S	G	G	F	I	P	K	P	R	F	S	W	L	E	N	G	R	-	-	L	P	C	187				
B7.2	115	K	P	T	G	S	I	L	O	O	T	L	T	E	S	V	I	A	N	F	S	E	P	-	-	-	-	-	-	-	-	-	-	-	-	E	I	K	L	A	Q	N	V	T	G	N	S	G	I	N	T	G	T	S	K	Q	C	H	I	P	K	P	K	K	M	Y	F	L	I	T	N	S	-	T	N	E	Y	G	181		
B7h	143	N	T	A	-	-	-	-	-	-	-	-	-	-	E	L	V	K	I	L	E	E	V	R	L	R	V	A	A	N	F	S	T	P	V	I	S	T	S	D	S	S	N	E	P	Q	-	E	R	T	Y	T	C	M	S	K	N	G	Y	P	E	N	L	Y	W	I	N	T	T	D	N	S	L	I	D	T	A	210			
PD-L1	119	G	Q	A	-	-	-	-	-	-	-	-	-	-	D	Y	K	R	I	T	L	K	N	A	P	Y	R	K	-	-	-	-	-	-	I	N	Q	R	I	S	V	D	P	A	T	S	E	H	E	L	I	C	Q	A	-	E	G	Y	P	E	A	E	V	I	W	T	N	S	D	H	Q	-	-	P	V	S	G	176			
PD-L2	107	G	A	A	W	-	-	-	-	-	-	-	-	-	D	Y	K	Y	L	T	V	K	N	A	S	Y	M	R	-	-	-	-	-	-	I	D	T	R	I	L	E	V	E	P	G	T	G	E	V	Q	L	T	C	Q	A	-	R	G	Y	P	L	A	E	S	W	Q	N	-	-	-	-	-	-	V	S	V	160				
B7-H3	127	Q	D	F	-	-	-	-	-	-	-	-	-	-	D	S	A	A	V	S	T	Q	V	A	P	Y	S	K	P	-	-	-	-	-	S	M	T	L	E	P	N	K	D	L	R	P	G	N	-	M	V	T	I	F	C	S	S	Y	Q	G	Y	P	E	A	E	V	F	W	K	D	G	Q	G	V	-	-	P	L	T	G	188

[illegible]

B7x	258	-PSPCVFSSAFAAG-W-ALLSLSCCL-----MLR	283
B7.1	256	GAVITVVVVIKCECKHRSCFRNEASRETNS-----LTFGPEEALAEQTVFL	306
B7.2	251	-TVALLLVMILIVCHKKPNQPSRPSTASKLERDSN-----ADRETINLKELFPQIASAKPNAE	309
B7h	282	-VPVLAVLA ^{AAAE} VSE-IITYRRTRPHRSYTG-----PKTVQLLELTDHAN	323
PD-L1	248	-LFLINVS ^T VL ^L LRK-QVRMLDVEK--CGVEDTS-----SKNRNDTQFFET	290
PD-L2	225	-VFIPACTI ^{II} ILL---AJVIIQRKR--I	247
B7-H3	257	-VCLVLLVLA ^E VGW-RKIKQSCEEENSGAEDQDGDGEGSKTALRPLKPSENKEDDGQFI A	316

FIGURE 5

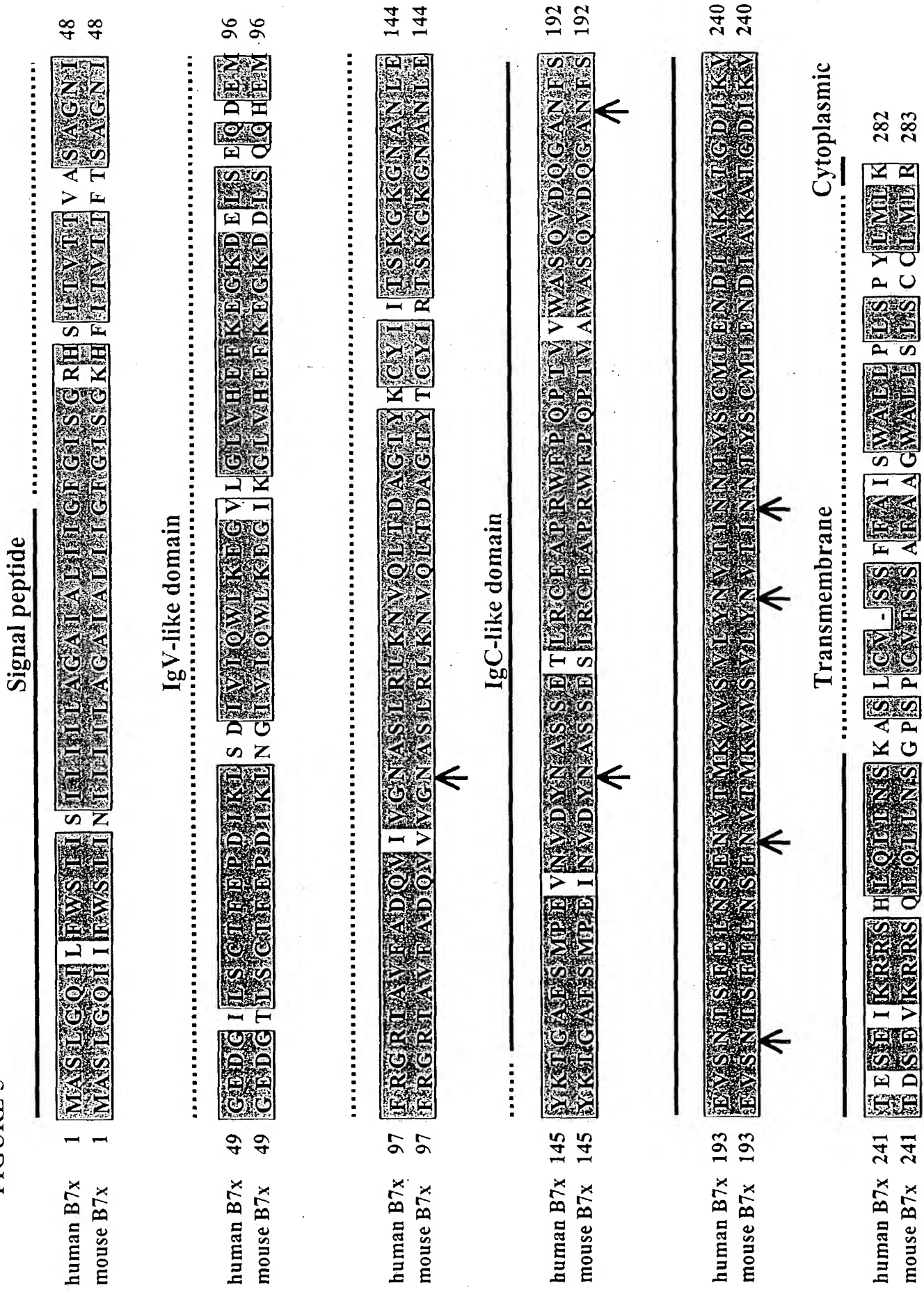


FIGURE 6

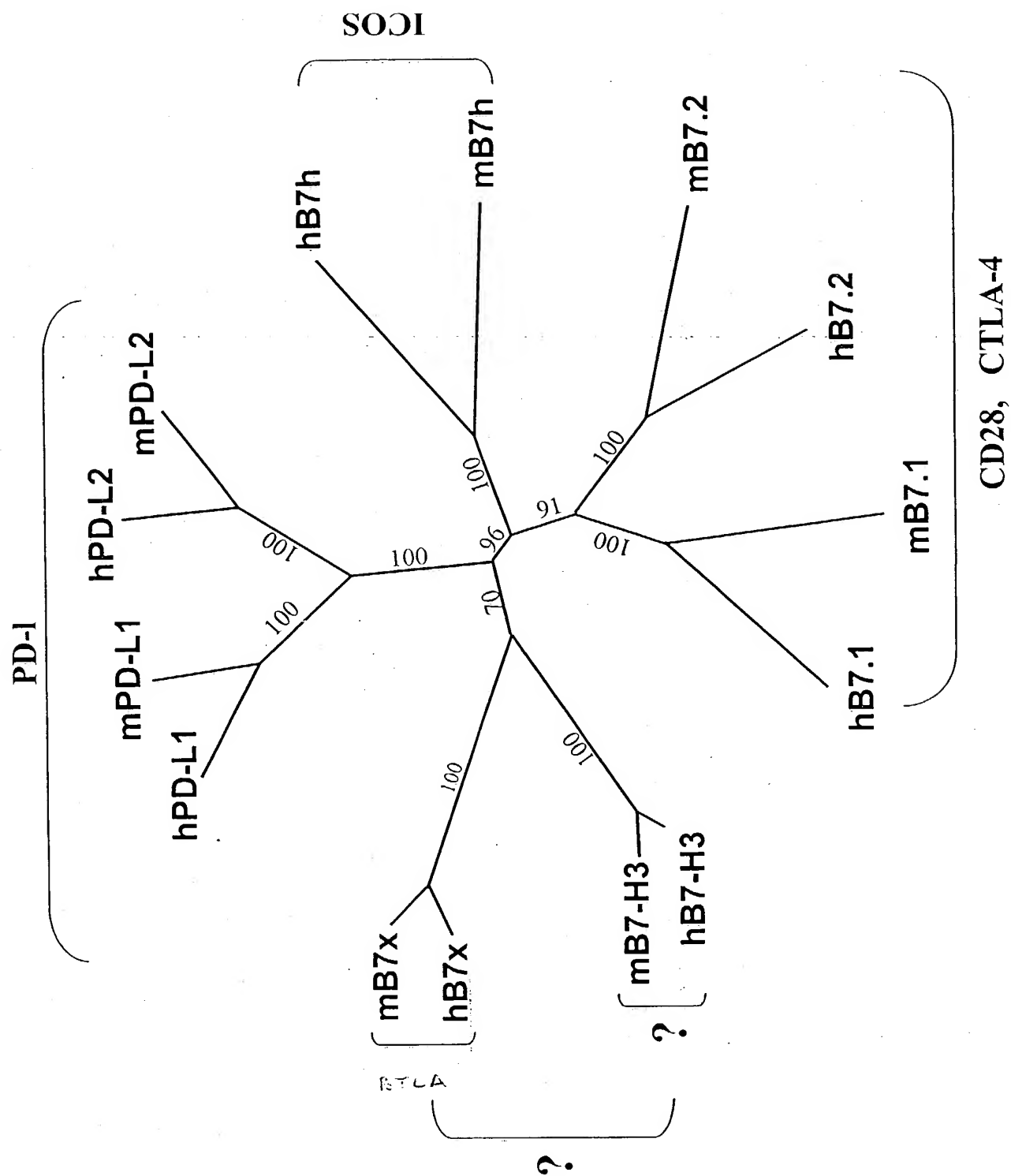


FIGURE 7

Human

Murine

PBL
Lung
Placenta
Small intestine
Liver
Kidney
Spleen
Thymus
Colon
Skeletal muscle
Heart
Brain

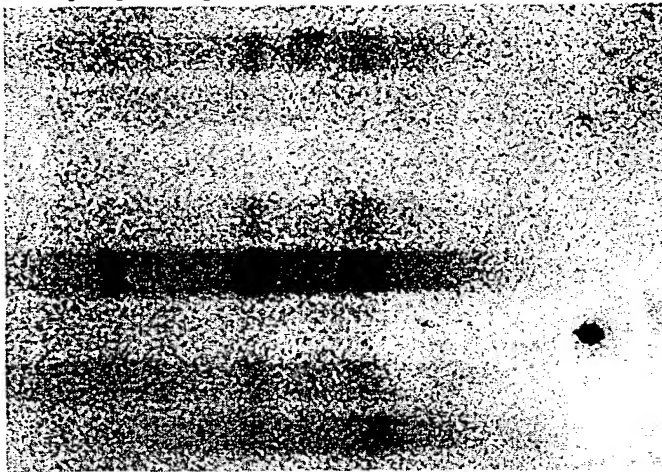
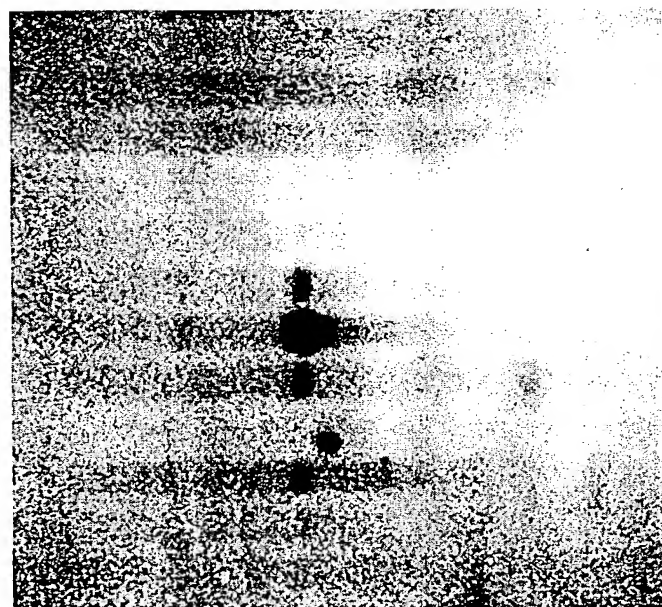
Testis
Kidney
Skeletal muscle
Liver
Lung
Spleen
Brain
Heart

9.5 —
7.5 —
4.4 —
2.4 —
1.35 —
0.24 —

— 9.5
— 7.5
— 4.4
— 2.4
— 1.35
— 0.24

B7x

Actin



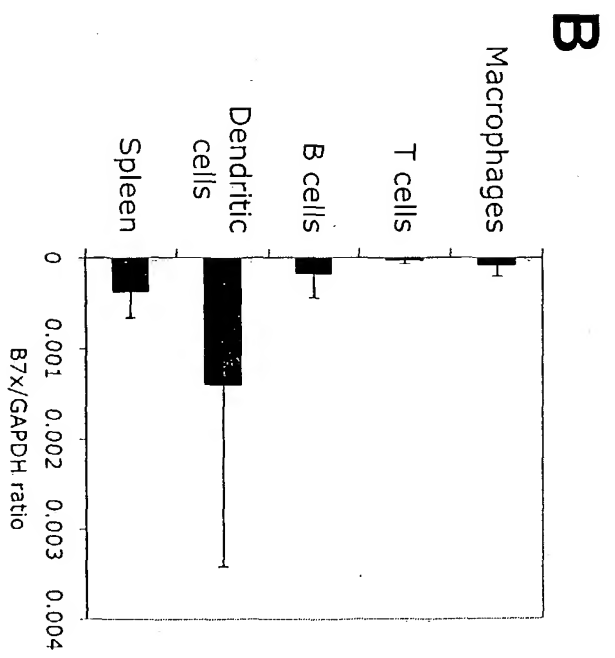
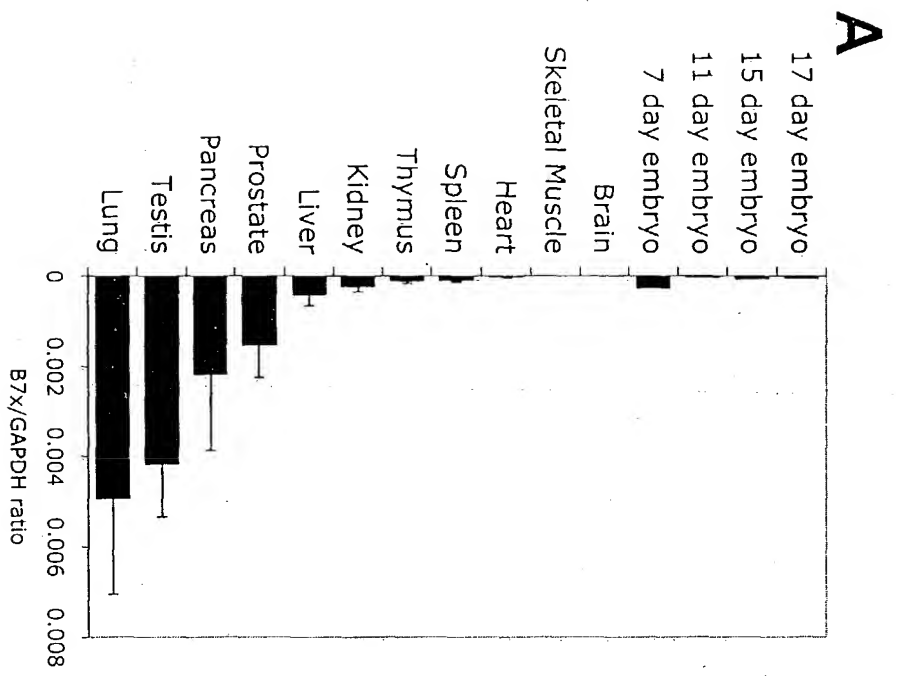


FIGURE 8

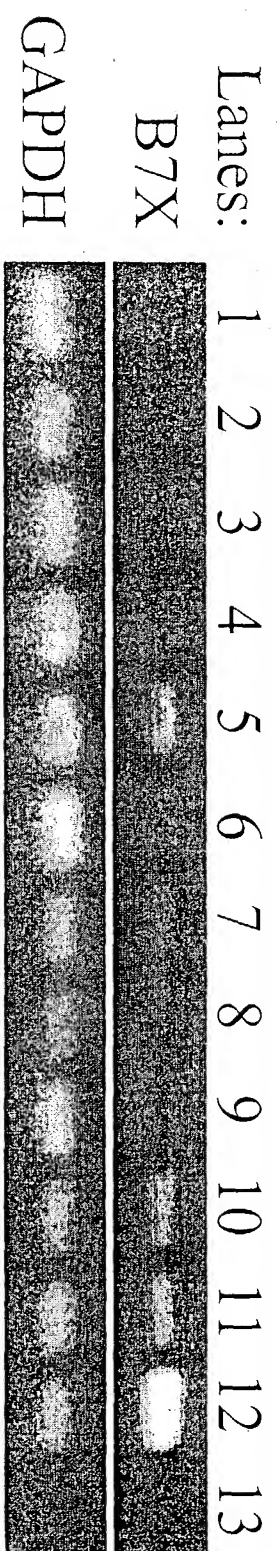


FIGURE 9

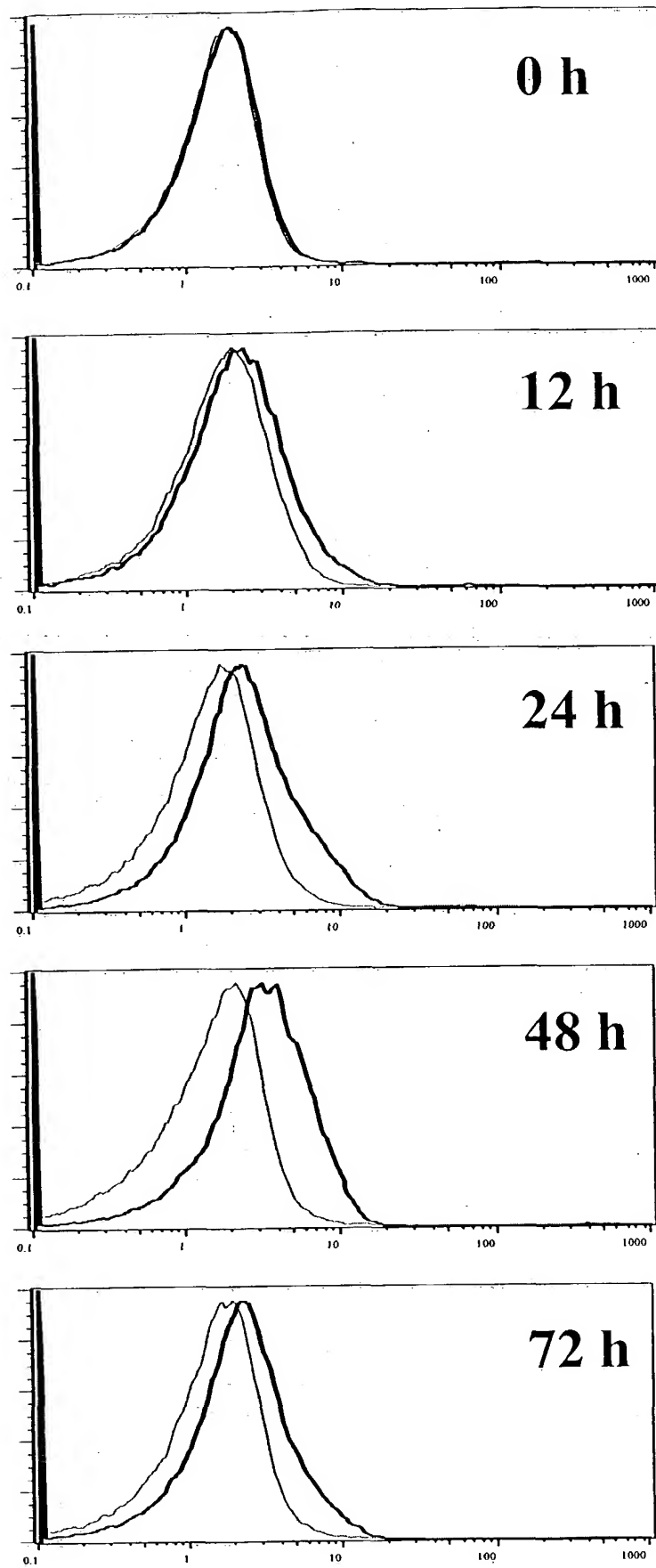


FIGURE 10

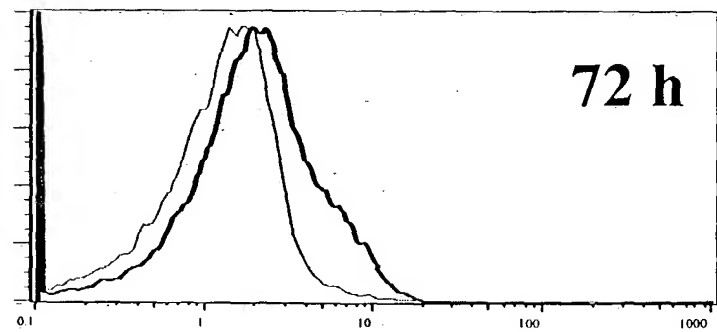
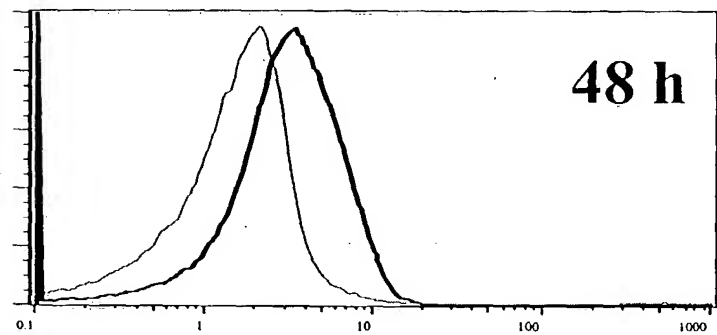
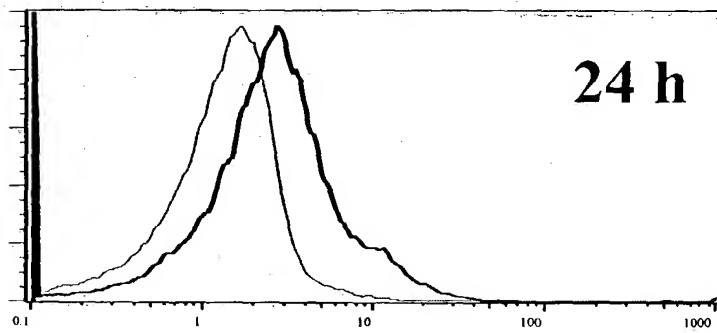
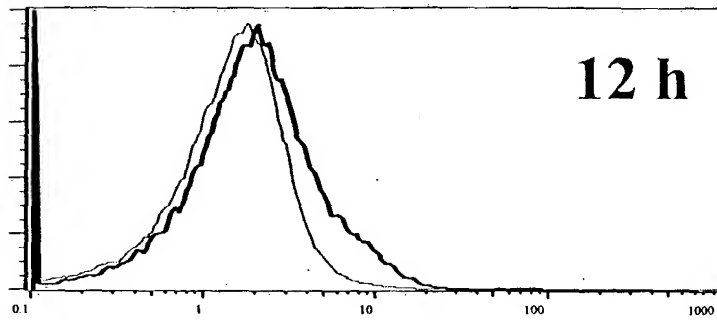
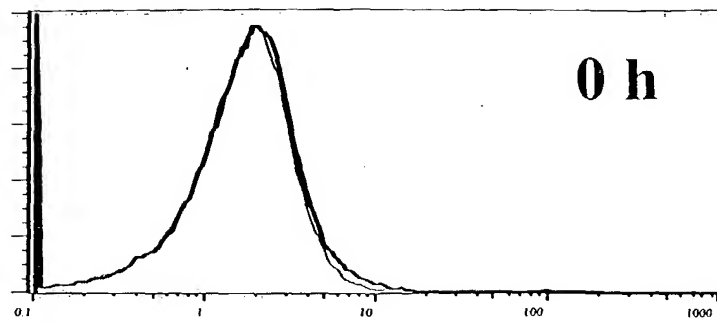
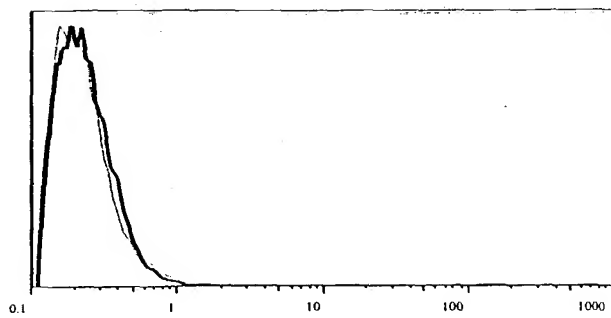
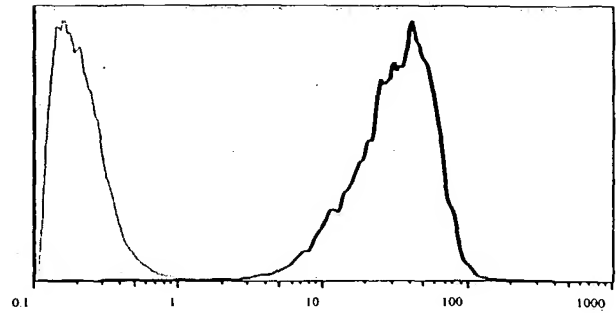


FIGURE 11

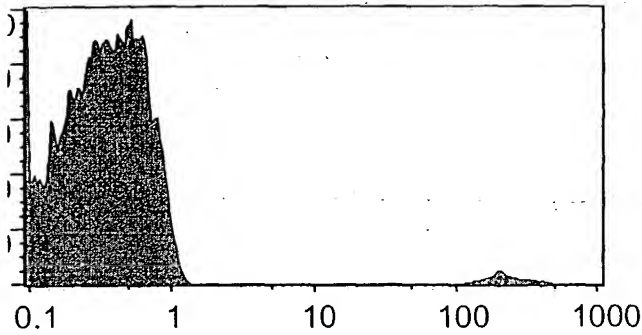
FIGURE 12



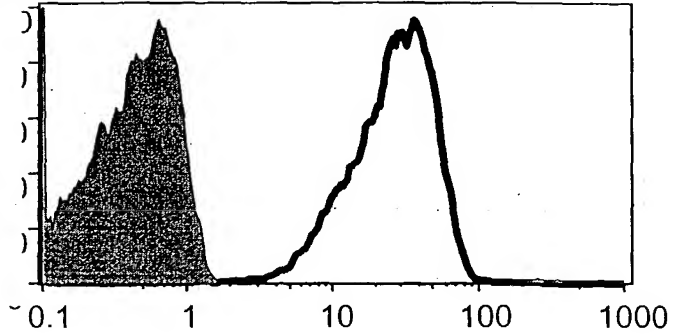
B7x-Ig



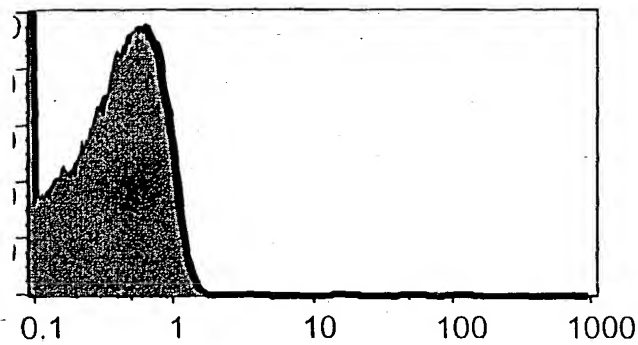
Anti-CD28



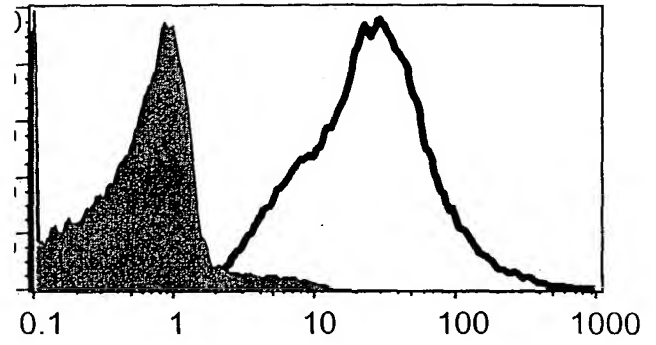
B7x-Ig



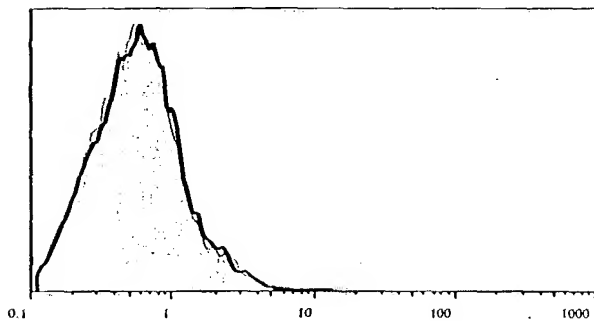
Anti-ICOS



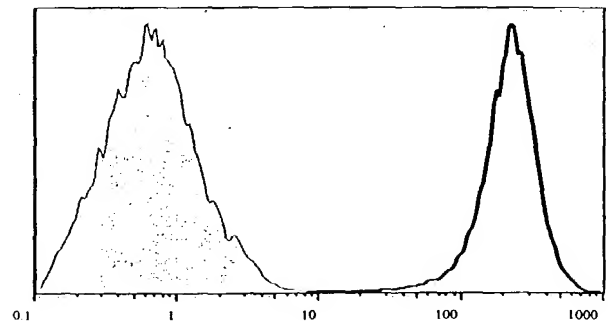
B7x-Ig



Anti-PD-1



B7x-Ig



Anti-CTLA-4

FIGURE 13A

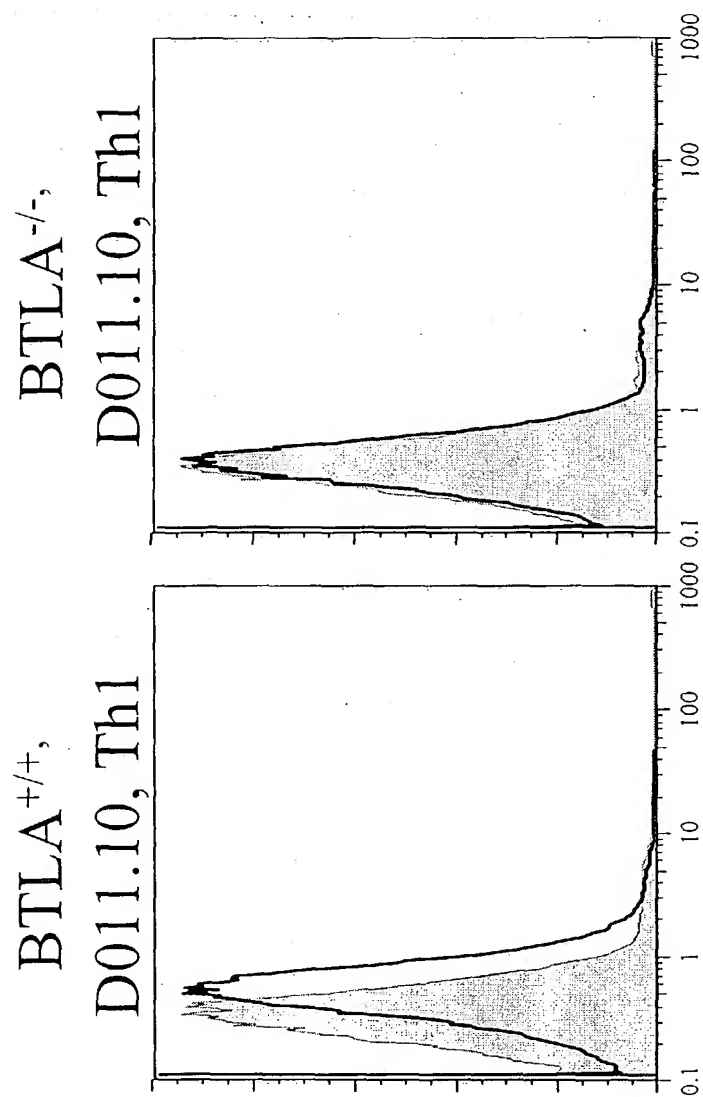


FIGURE 13B

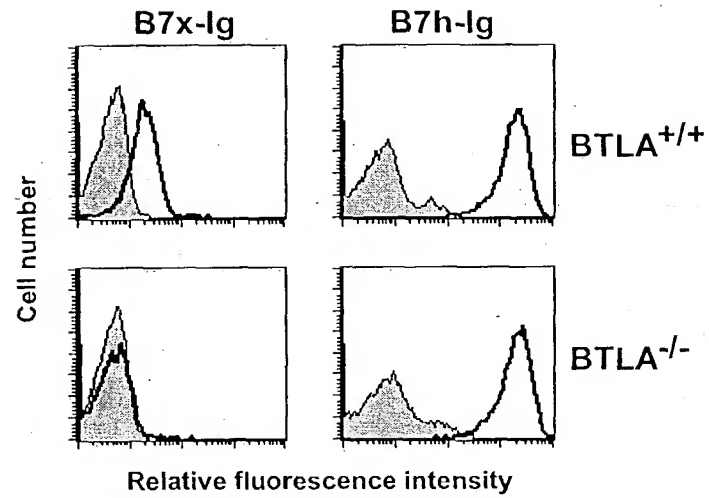
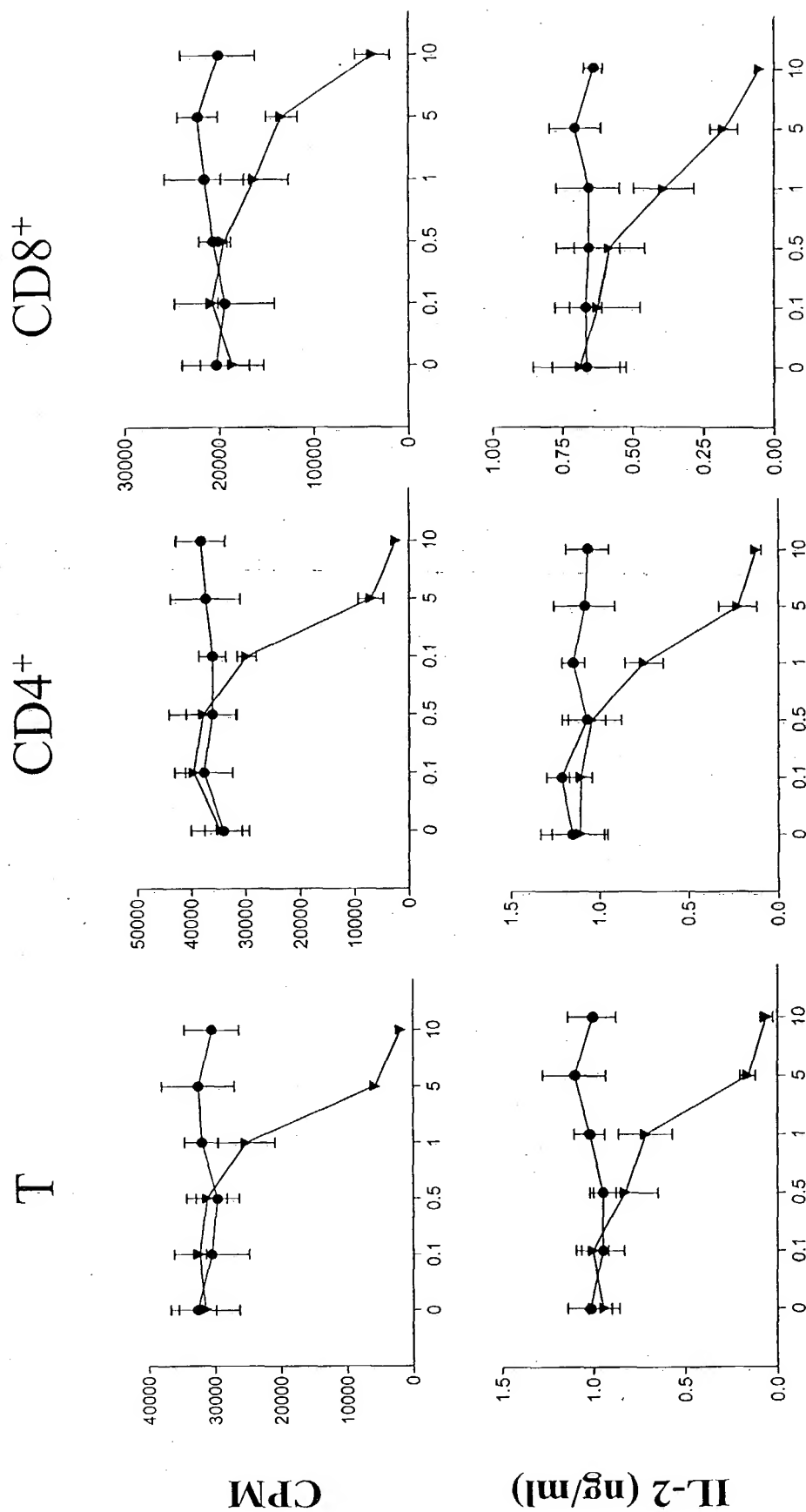


FIGURE 14



Ig concentration (ug/ml)

FIGURE 15

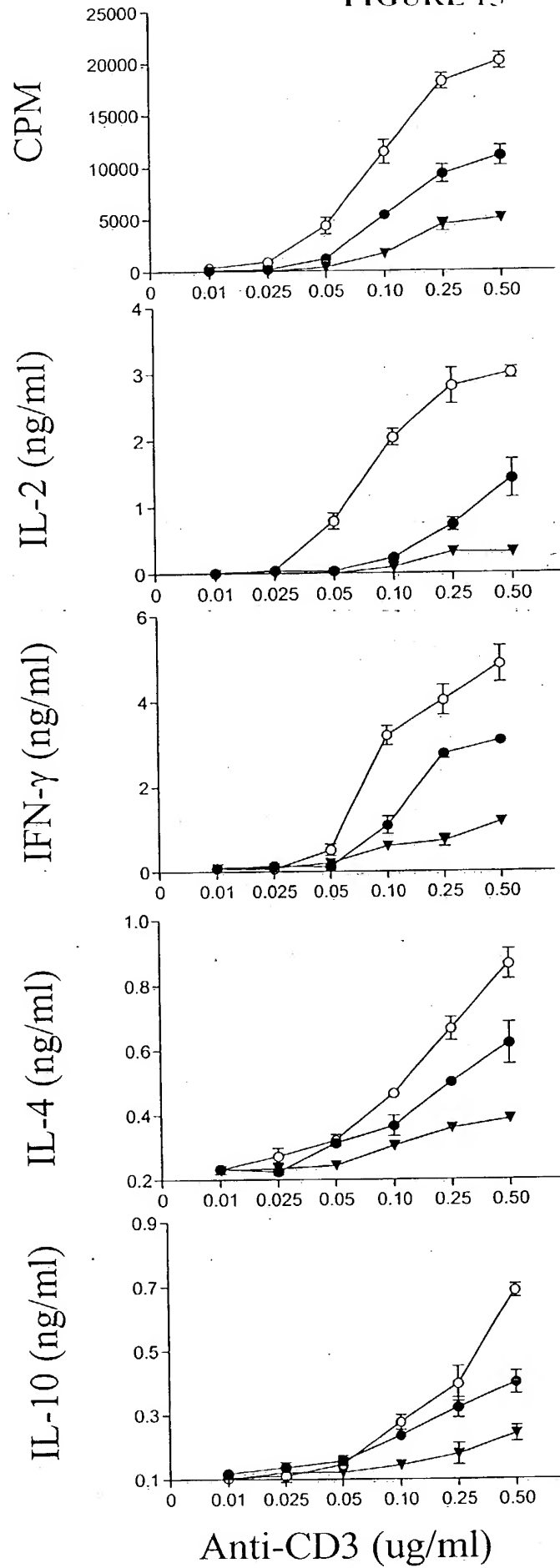


FIGURE 16

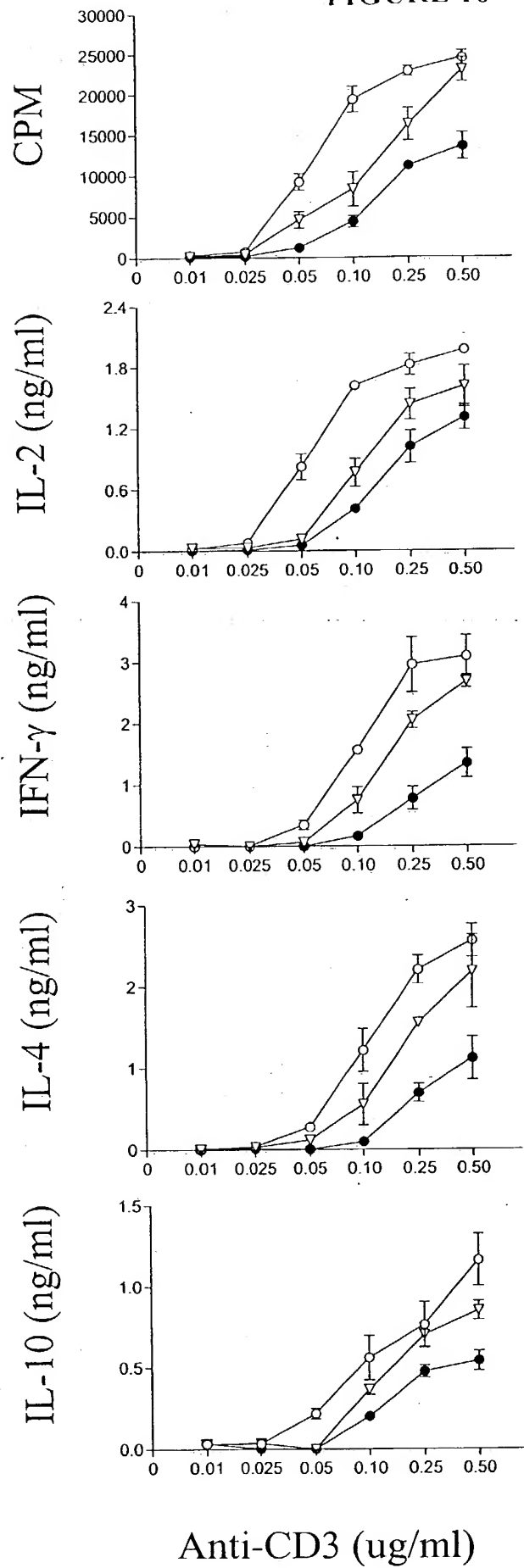
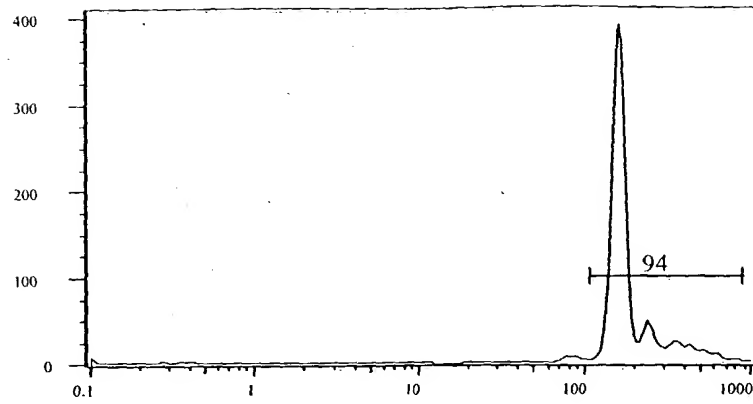
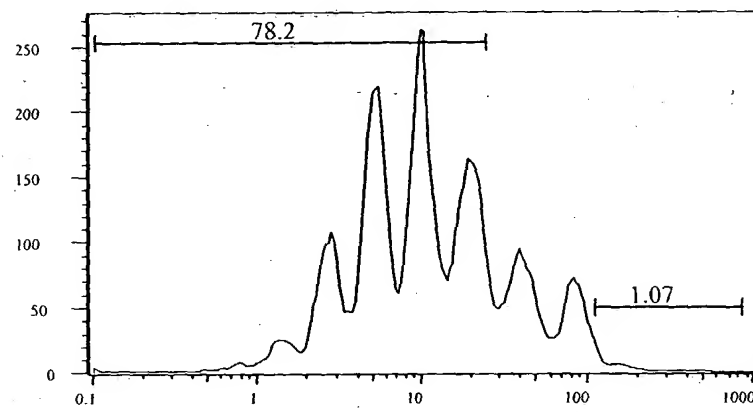


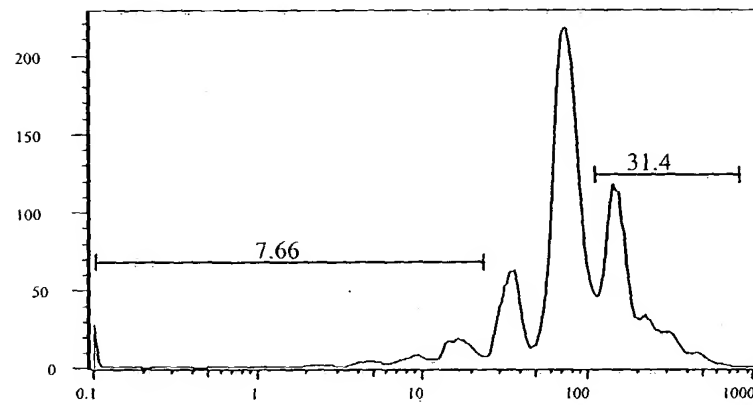
FIGURE 17



GFP/CHO



GFP/CHO + anti-CD3



B7x/CHO + anti-CD3

FIGURE 18

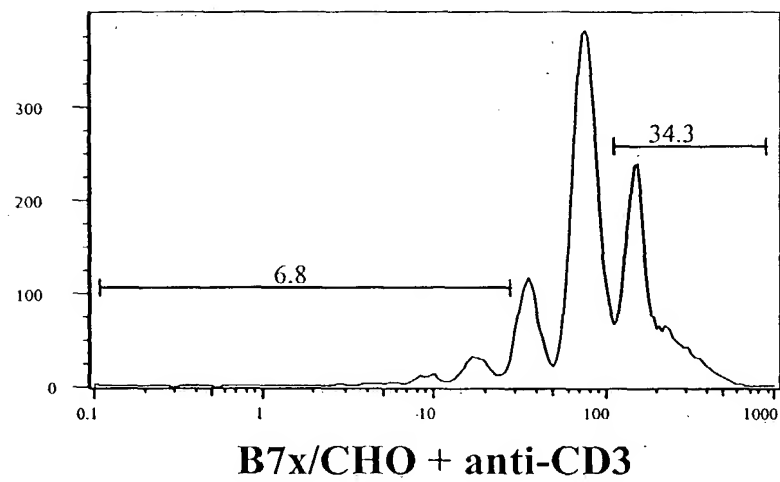
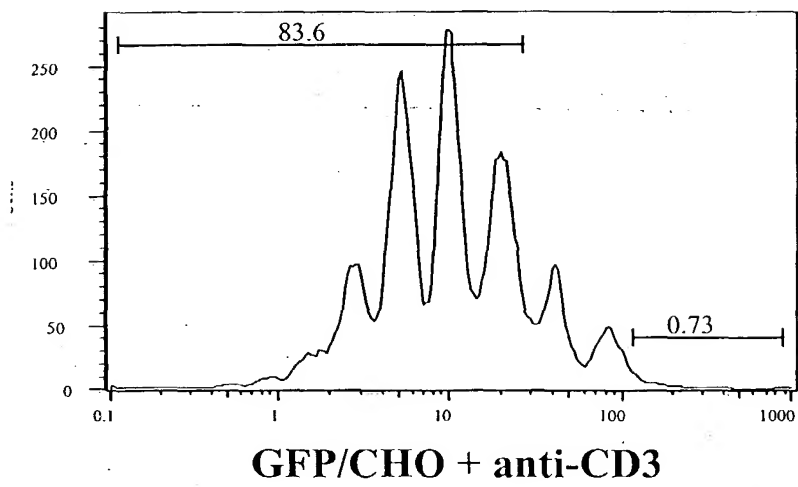
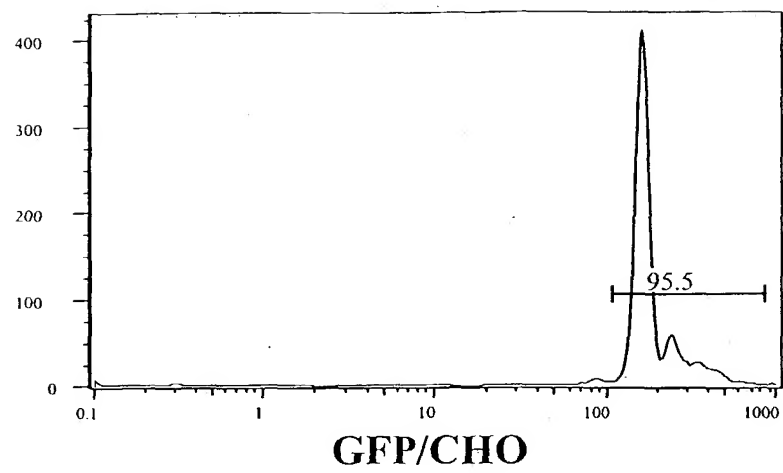


FIGURE 19

```

mouse BTLA 1 MKTVPAMLGTPRLFREFFIL•HLGLWSILCEKATKRNDEE
human BTLA MKTLPAMLGTGKLFVFFLIPYLDIWNI••••••••HGKES

      40 CEVQLNIKRNSKHS•AWTGELFKIECPVKYCVHRPNVTWCK
          CDVQLYIKRQSEHSILAGDPFELECPVKYCANRPHVTWCK

      80 HNGTIWVPLEVGPQLYTSWEENRSVPVFVLHFKPIHLSDN̄
          LNGTTCVKLEDR•Q••TSWKEEKNISFFILHFEPVLPNDN

     120 GSYSC̄STNFNSQVINSHSVTIHVRERTQ̄NSSEHPLITVSD
          GSYRCSANFQSNLIESHSTTLYVTDVKSAS••••••••

     160 IPDATN̄ASGPSTMEERPGRTWLLYTLLPLGALLLLL•ACV
          ••••••••ERPSKDEMAS•RPWLLYSLLPLGGLPLLITTCF

     199 CLLCFLKRIQGKEKKPSDLAGRDTNLVD••••••••IPASS
          CLFCCLRRHQKGQNELSDTAGREINLVDAHLKSEQTEAST

     232 RTNHQALPSGTGIYDND•WSS••MODESELTISLQSERNN
          RQNSQVLLSETGIYDND•DLCFRMQEGSEVYSNPCLEENK

     270 QGIVYASLNH•CVIGRNPRQENNMQ•EAPTEYASICVRS
          HGIVYASLNH•SVIGLNSRLARNV•EAPTEYASICVRS
  
```

FIGURE 20

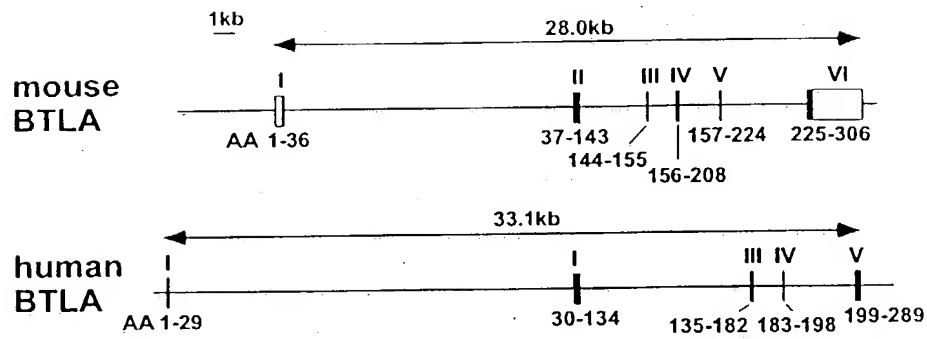
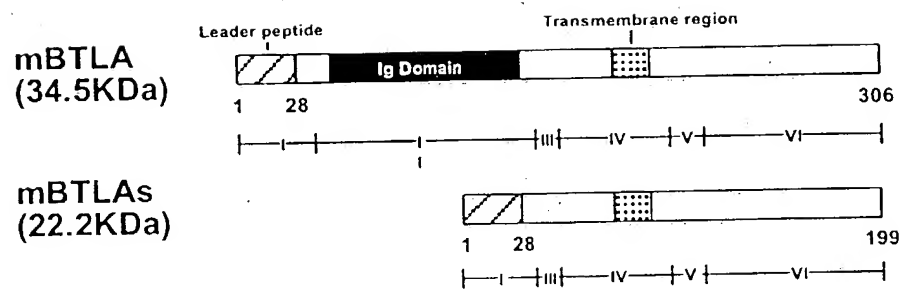


FIGURE 21



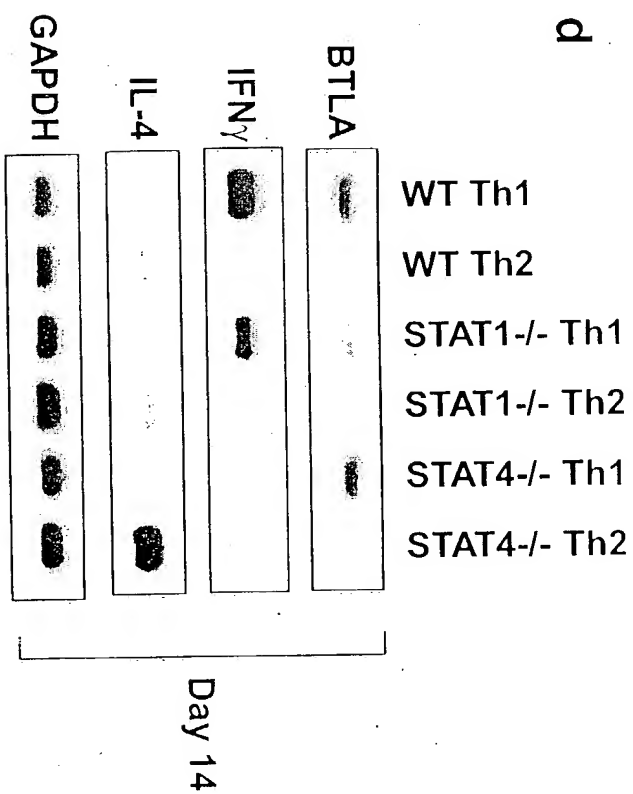
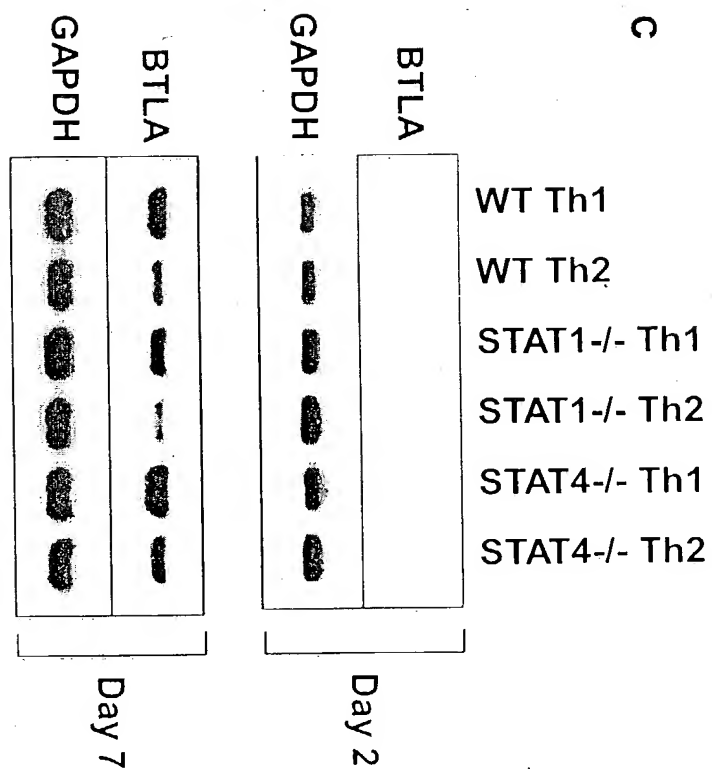
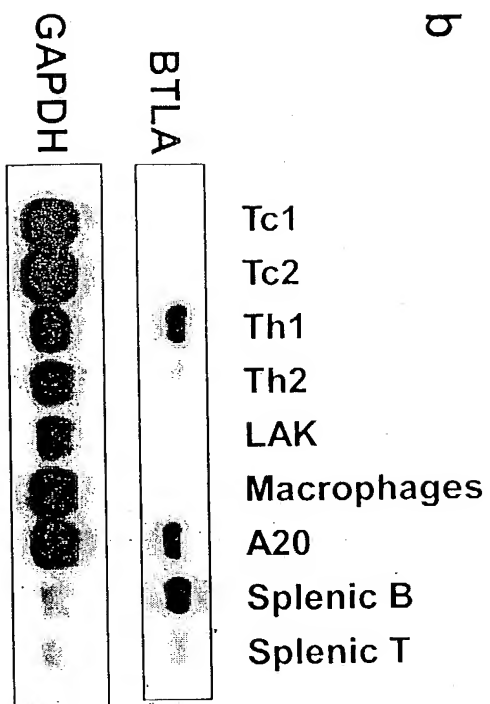
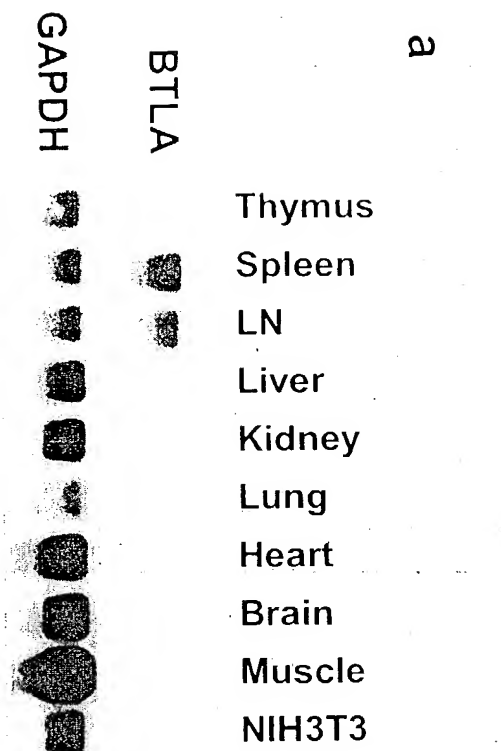


FIGURE 22

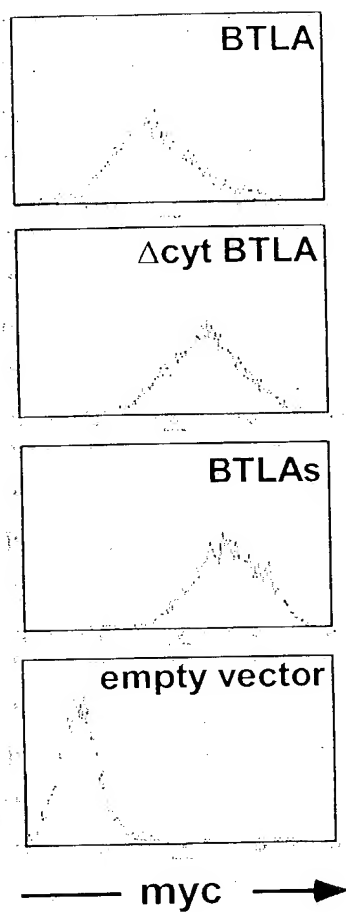
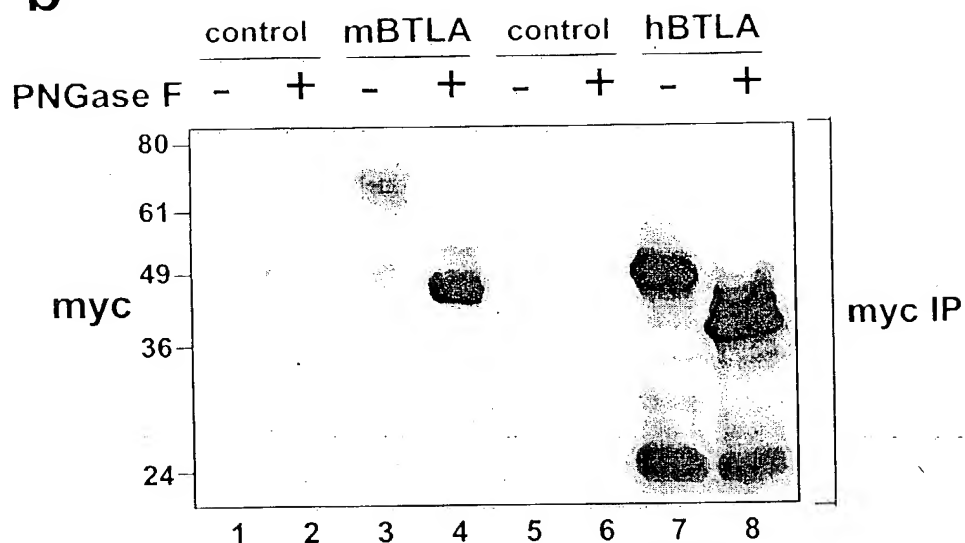
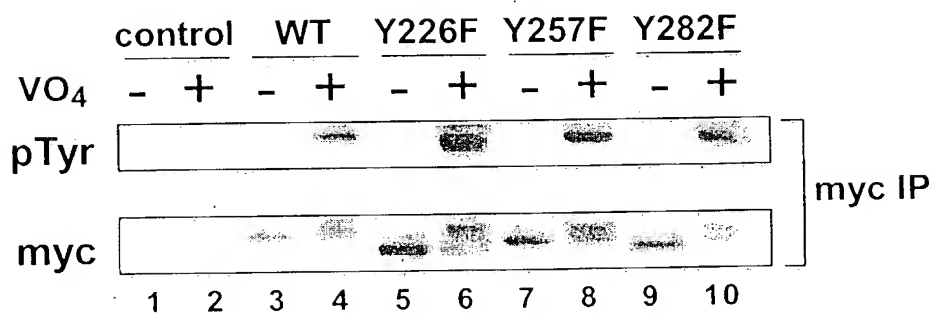
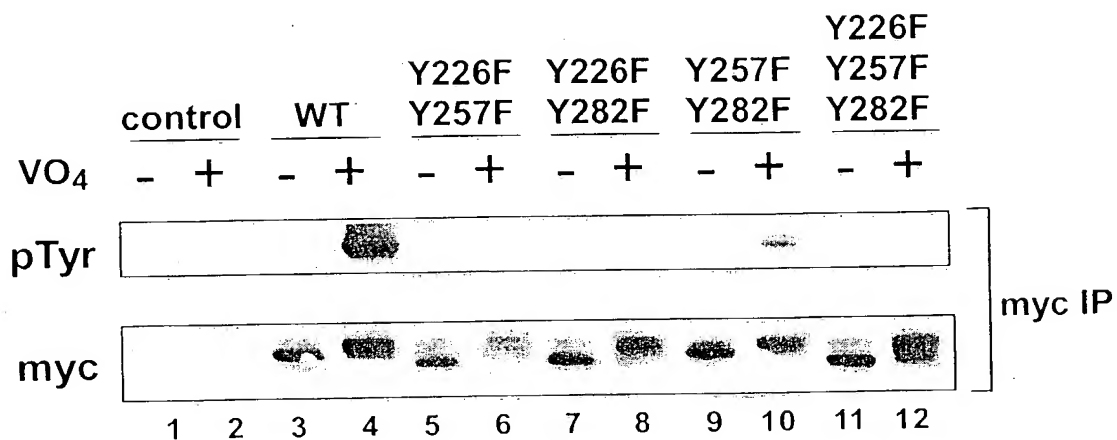
a**b****c****d**

FIGURE 23

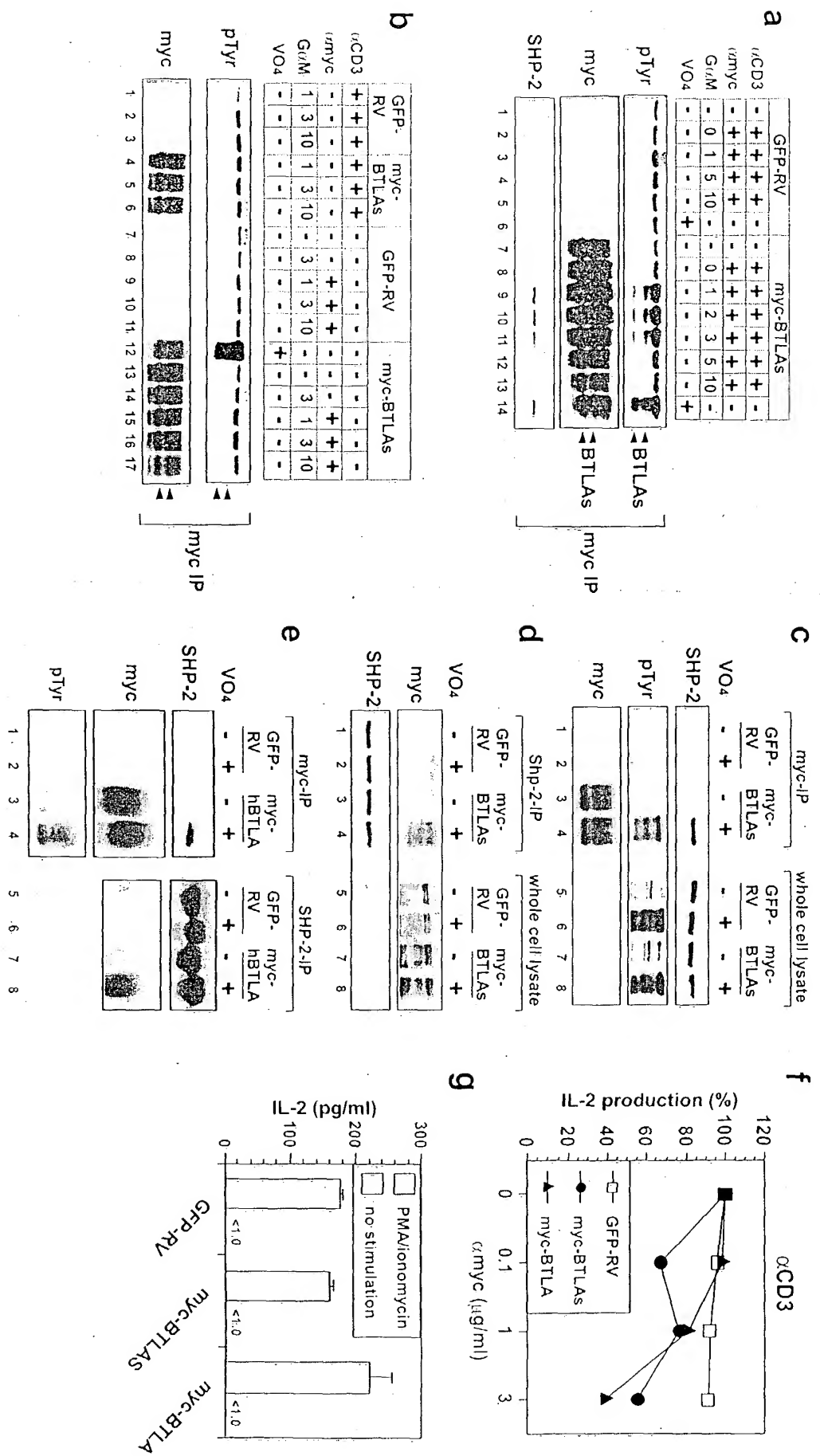


FIGURE 24

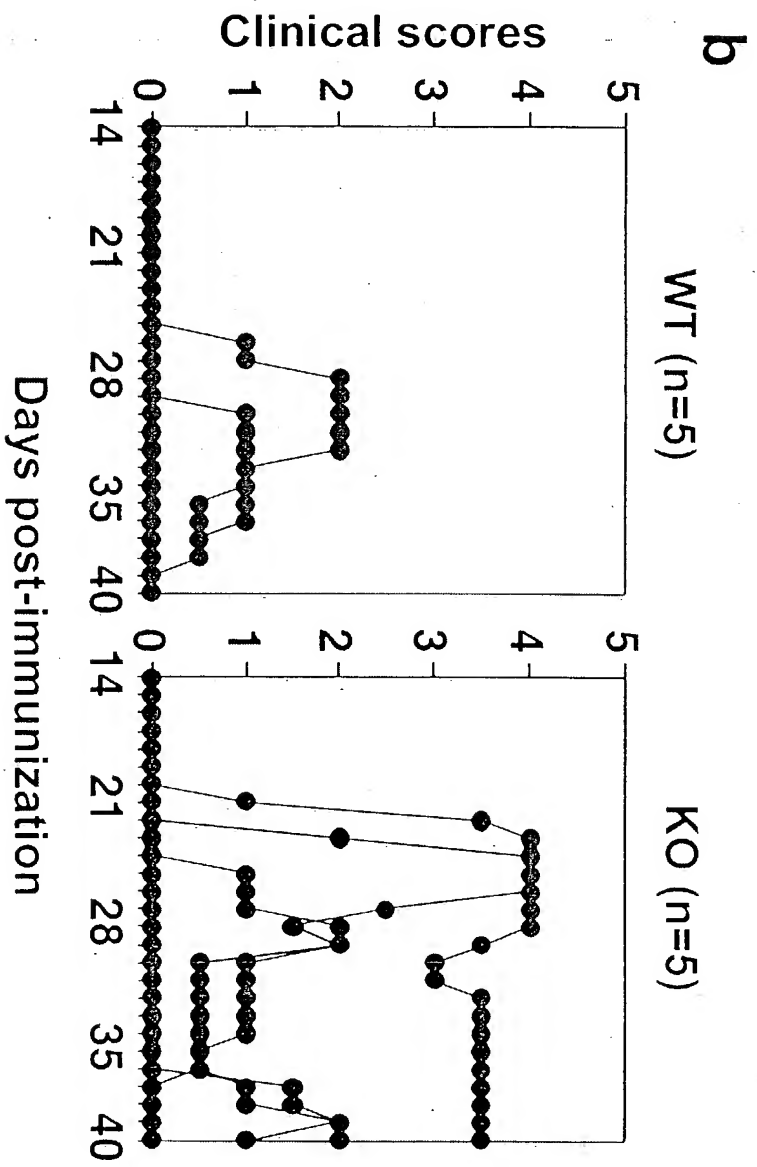
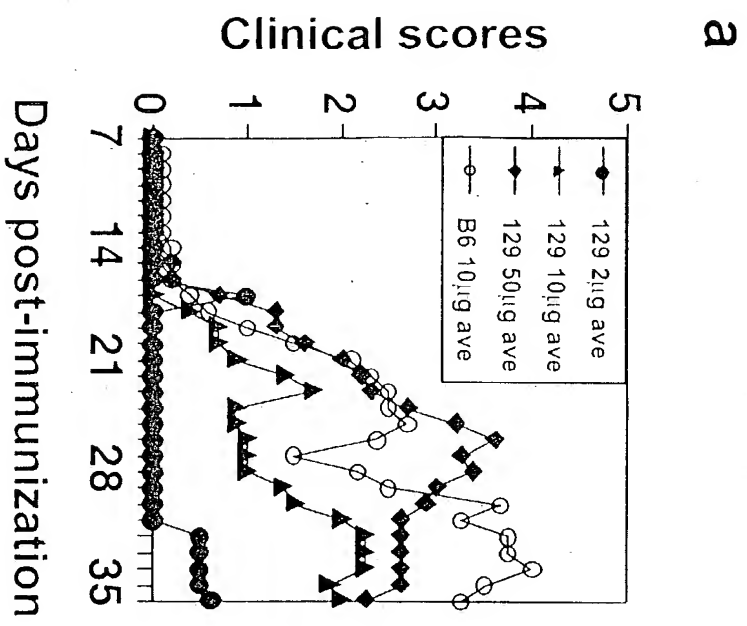


FIGURE 26

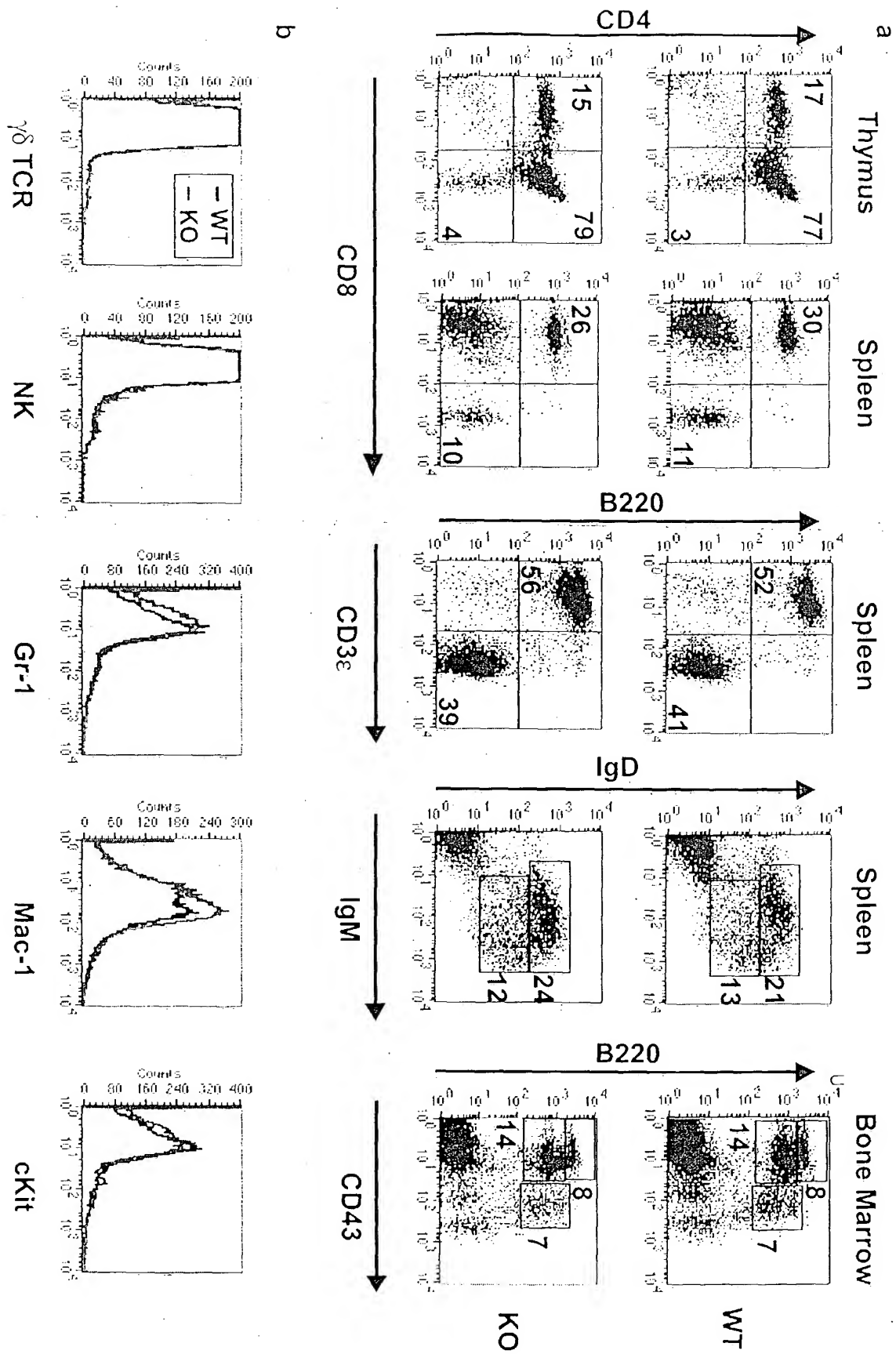


FIGURE 27

HUMAN BTLA PROTEIN SEQUENCE

```

1   mktlpamlgt gklfwvffli pyldiwnihg kescdvqlii krgsehsila
51  gdpfelecpv kycaurphvt wcklngttcv kledrqtswk eeknisffil
101 hfepmlpndn gsyrcsanfg snlieshstt lyvtdvkgas erpskdevas
151 rpwllyslip lgglpllitt wfclfcclrr hggkqnelds tagreinlvd
201 ahlkseqtea strqnsqvll seagiydndp dlcfmqegs evcsnplee
251 nkpgivyasl nhsviglusr larnvkeapt eyasicvrs

```

HUMAN BTLA NUCLEIC ACID SEQUENCE

```

1   atgaagacat tgccctgccat gcttggaact gggaaattat tttgggtctt ctctttaatc
61  ccatatctgg acatctggaa catccatggg aaagaatcat gtgatgtaca gctttatata
121 aagagacaat ctgaacactc catcttagca ggagatccct ttgaactaga atgcctctgt
181 aaatactgtg ctaacaggcc tcatgtgact tgggtgcaagc tcaatggaac aacatgtgta
241 aaacttgaag atagacaaac aagttggaag gaagagaaga acatttcatt tttcattcta
301 ctttttgaac caatgcttcc taatgacaat gggtcatacc gctgttctgc aaattttcag
361 tctaactctc ttgaaagcca ctcaacaact ctttatgtga cagatgtaaa aggtgcctca
421 gaacgaccct ccaaggacga agtggcaagc agaccctggc tcctgtatag tttacttcct
481 ttgggggggat tgccctctact catcactacc tggttctgcc tgttctgetg cctgagaagg
541 caccaaggaa agcaaaatga actctctgac acagcaggaa gggaaattaa tctggttgat
601 gctcacctta agagcgagca aacagaagca agcaccaggc aaaattccca agtactgcta
661 tcagaagctg gaatttatga taatgacctt gacctttgtt tcaggatgca ggaagggctt
721 gaagtttgtt ctaatccatg cctggaagaa aacaaaccag gcattgttta tgcttccttg
781 aaccattctg tcattggact gaactcaaga ctggcaagaa atgtaaaaga agcaccaaca
841 gaatatgcat ccatatgtgt gaggagttaa

```

FIGURE 28

MOUSE BTLA PROTEIN SEQUENCE

```

1  mktvpamlgt prlfreffil hlglsilce katkrndeec evqlnikrns khsawtgelf
61  kiecgvkykv hrpnvtwckh ngtiwvplev gpqlytswee nrsvpvfvlh fkpihlndng
121 syscstnfns qvinshsvti hvrrertqnss ehplltvsdi pdatnasgps tmeerpgrtw
181 llytllplga lllllacvcl lcflkriqgk ekkpsdlaqr dtnlvdipas srtnhqalps
241 gtgiydndpw ssmqdeselt islqsernnq givyaslnhc vigrnprqen nmqeapteya
301 sicvrs

```

MOUSE BTLA NUCLEIC ACID SEQUENCE

```

1  atgaagacag tgcctgccat gcttgggact cctcgggttat ttaggggaatt cttcactctc
61  catctggggc tctggagcat cctttgtgag aaagctacta agaggaatga tgaagagtgt
121 gaagtgcac ttaatatata gaggaattcc aaacactctg cctggacagg agagtatttt
181 aaaattgaat gtctgtgaa atactgtgtt catagacctt atgtgacttg gtgtaagcac
241 aatggaacaa tctgggtacc ccttgaagtt ggtcctcagc tatacactag ttgggaagaa
301 aatcgatcag ttccgggttt tgttctccat tttaaaccac tacatctcag tgataacggg
361 tcgtatagct gttctacaaa cttcaattct caagttatta atagccattc agtaaccatc
421 catgtgagag aaaggactca aaactcttca gaacacccac taataacagt atctgacatc
481 ccagatgcca ccaatgcctc aggaccatcc accatggaag agaggccagg caggacttgg
541 ctgctttaca ccttgcttcc tttgggggca ttgcttctgc tccttgcttg tgtctgcttg
601 ctctgcttcc tgaaaaggat ccaagggaaa gaaaagaagc cttctgactt ggcaggaagg
661 gacactaacc tgggtgatat tccagccagt tccaggacaa atcaccaagc actgccatca
721 ggaactggaa tttatgataa tgatccctgg tctagcatgc aggatgaatc tgaattgaca
781 attagcttgc aatcagagag aaacaaccag ggcattgttt atgcttcttt gaaccattgt
841 gttattggaa ggaatccaag acaggaaaac aacatgcagg aggcacccac agaatatgca
901 tccatttgtg tgagaagtta a

```

FIGURE 29

Section 1

	(1)	1	10	20	30	40	57
129 SvJ	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
MRL/lpr (bc)	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
C57Bl/6	(1)	GATGAAGAGTGTCCAGT	GCAACTTACTATTACGAGGAATTCCAAACAGTCTGCCAGG				
Balb/c	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
SWR	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
NZB/BluJ	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
NOD	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
MRL/lpr	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
DBA/2J	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
C3H/J	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
129SvEv	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
SJL/J	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
Celera old	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
WEHI 2 old	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
Bl/6 old	(1)	GATGAAGAGTGTCCAGT	GCAACTTACTATTACGAGGAATTCCAAACAGTCTGCCAGG				
WEHI 1old	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
Consensus	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				

Section 2

	(58)	58	70	80	90	100	114
129 SvJ	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
MRL/lpr (bc)	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTCAT				
C57Bl/6	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
Balb/c	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
SWR	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTCAT				
NZB/BluJ	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
NOD	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
MRL/lpr	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTCAT				
DBA/2J	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTCAT				
C3H/J	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
129SvEv	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
SJL/J	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
Celera old	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
WEHI 2 old	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGGAATACTGTGTTTCATAGACCTCAT				
Bl/6 old	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
WEHI 1old	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGGAATACTGTGTTTCATAGACCTCAT				
Consensus	(58)	ACAGGAGAGTTATTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				

FIGURE 30

Section 3

	(115)	115	120	130	140	150	160	171
129 SvJ (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
MRL/lpr (bc) (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
C57Bl/6 (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
Balb/c (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
SWR (115)	CTGACTTCGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
NZB/BinJ (115)	CTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
NOD (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
MRL/lpr (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
DBA/2J (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
C3H/J (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
129SvEv (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
SJL.J (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
Celera old (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
WEHI 2 old (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
Bl/6 old (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
WEHI 1old (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	
Consensus (115)	GTGACTTGGT	GTAAGCACA	AATGGAACA	AATCTGGG	TACCCCTT	GAAAGTTGG	TCCCTCAG	

Section 4

	(172)	172	180	190	200	210	228
129 SvJ (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
MRL/lpr (bc) (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
C57Bl/6 (172)	CTATACACTAG	TTGGGAAGA	AAATCAAT	CAGTTCCGG	TTTTGTTCT	CCACTTTTAAA	
Balb/c (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
SWR (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
NZB/BinJ (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
NOD (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
MRL/lpr (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
DBA/2J (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
C3H/J (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
129SvEv (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
SJL.J (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
Celera old (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
WEHI 2 old (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
Bl/6 old (172)	CTATACACTAG	TTGGGAAGA	AAATCAAT	CAGTTCCGG	TTTTGTTCT	CCACTTTTAAA	
WEHI 1old (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	
Consensus (172)	CTATACACTAG	TTGGGAAGA	AAATCGAT	CAGTTCCGG	TTTTGTTCT	CCATTTTAAA	

FIGURE 30

	(229) 229	240	250	260	270	285
129 SvJ (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
MRL/lpr (bc) (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
C57Bl/6 (229)	CCAATACATCTCAGTGATAATGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
Balb/c (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
SWR (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
NZB/BinJ (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
NOD (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
MRL/lpr (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
DBA/2J (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
C3H/J (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
129SvEv (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
SJL.J (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
Celera old (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
WEHI 2 old (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
Bl/6 old (229)	CCAATACATCTCAGTGATAATGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
WEHI 1old (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
Consensus (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					

	(286) 286	300	310	322
129 SvJ (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
MRL/lpr (bc) (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
C57Bl/6 (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGACAG			
Balb/c (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
SWR (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
NZB/BinJ (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
NOD (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
MRL/lpr (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
DBA/2J (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
C3H/J (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
129SvEv (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
SJL.J (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
Celera old (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
WEHI 2 old (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
Bl/6 old (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGACAG			
WEHI 1old (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
Consensus (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			

FIGURE 30

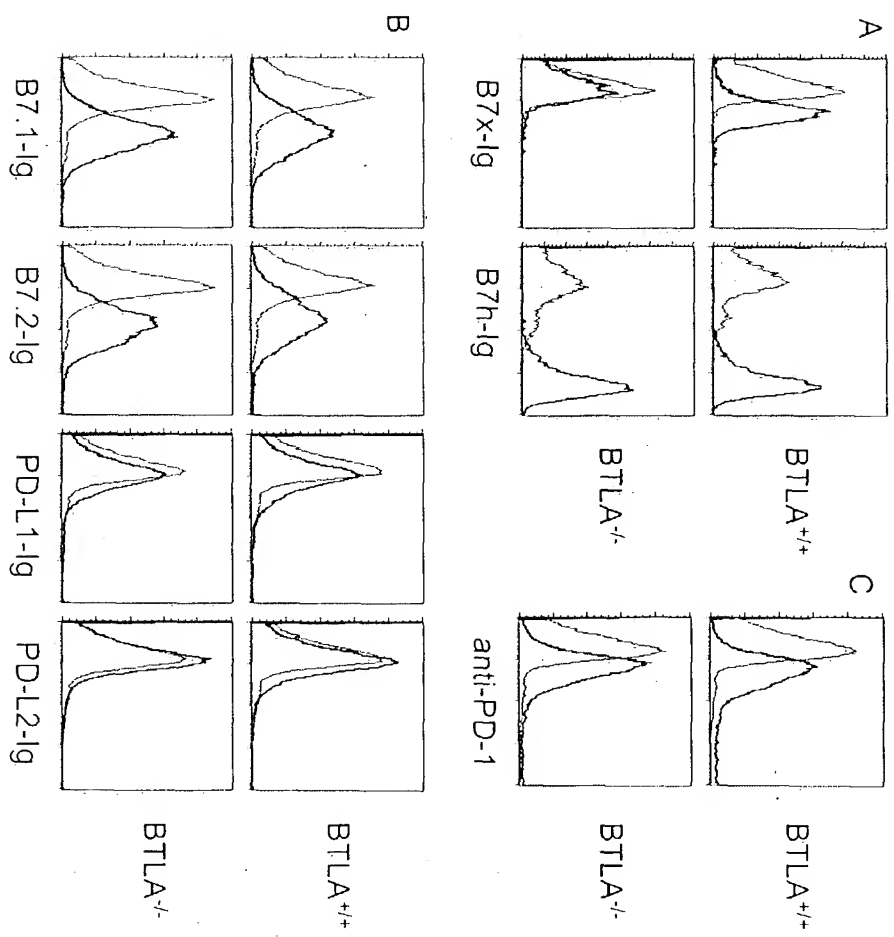
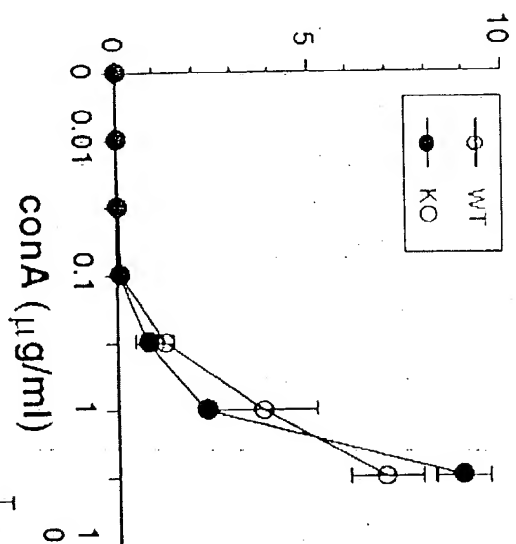


FIGURE 31

T cells



B cells

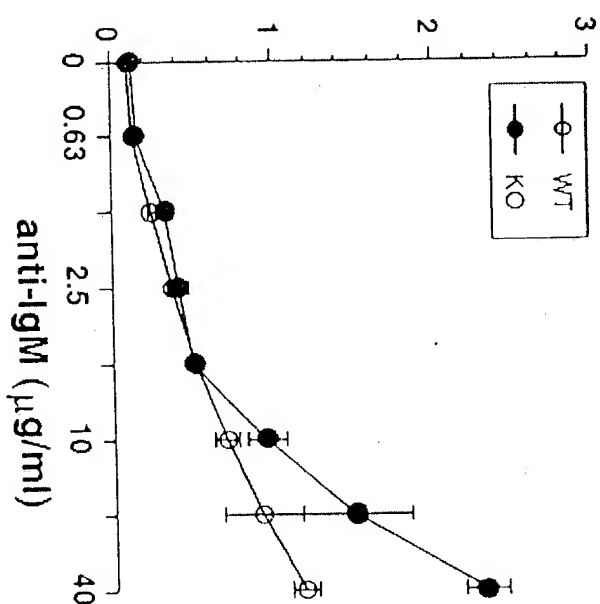
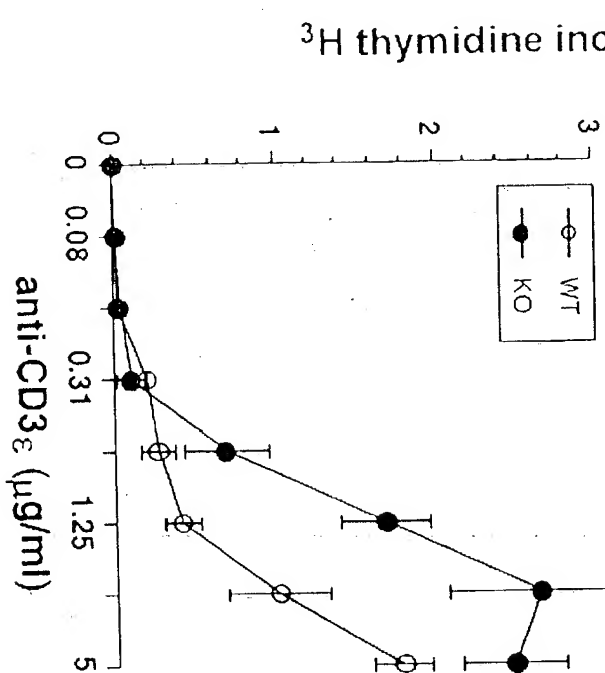
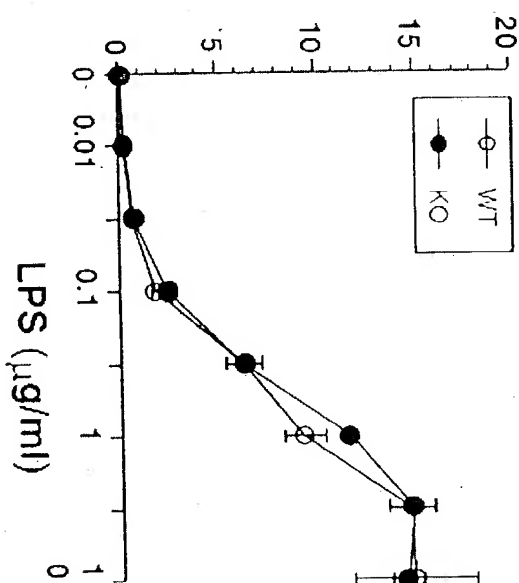


FIGURE 32